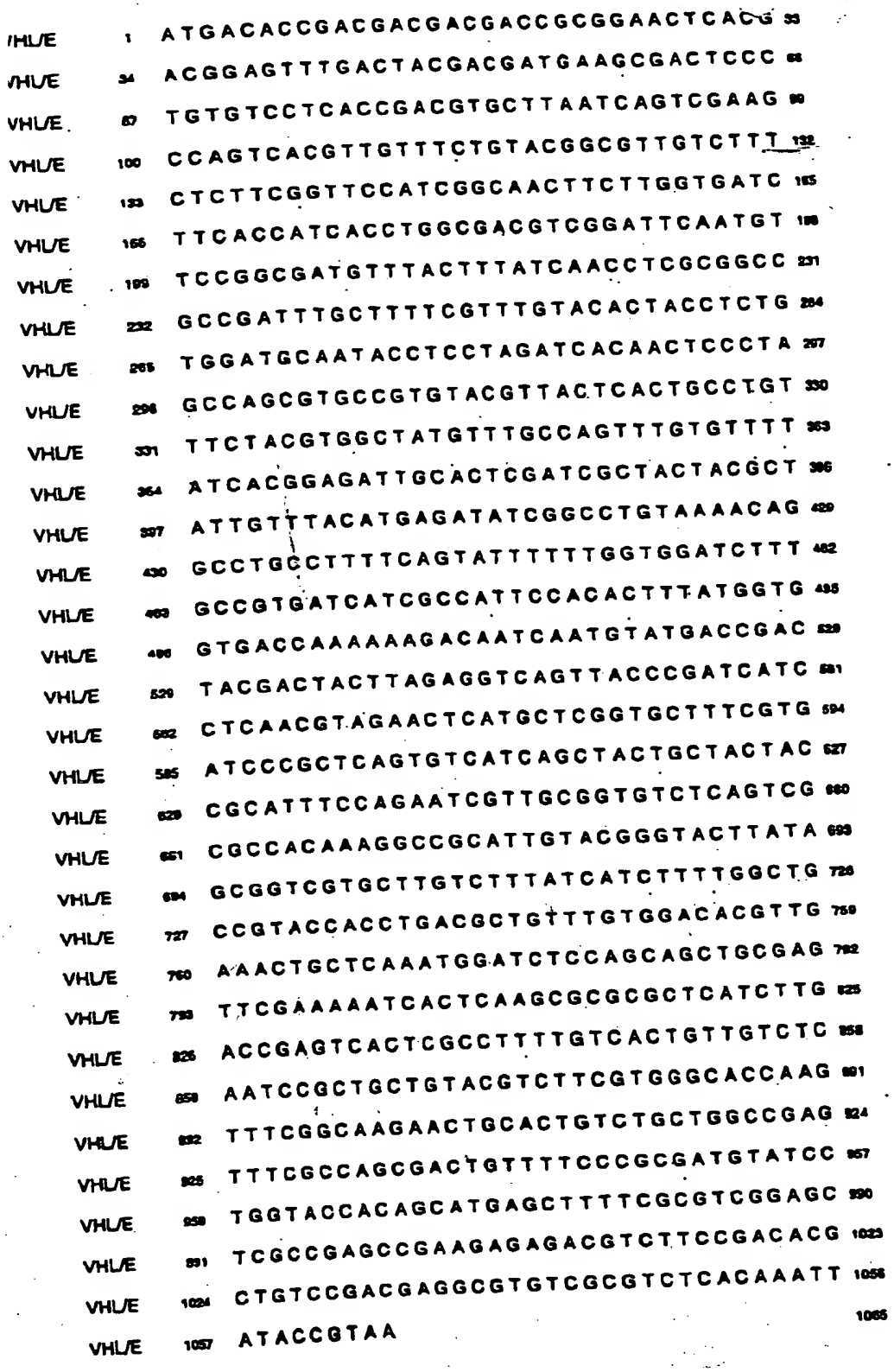
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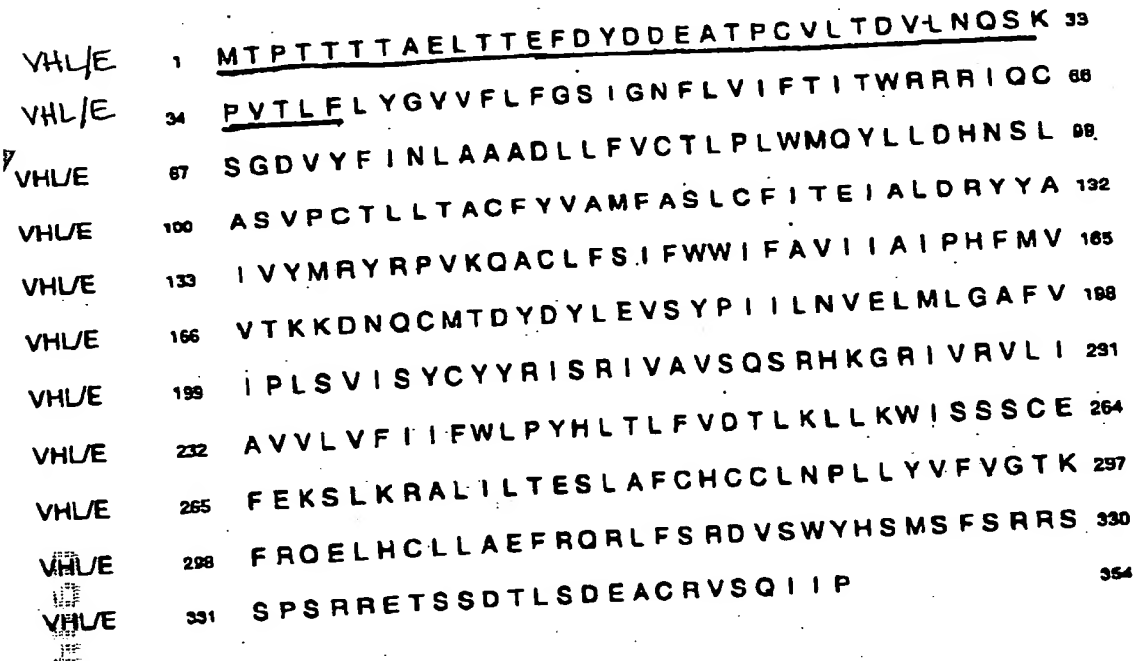
VHL/E 34 ACGGAGTTTGACTACGACGATGAAGCGACTCCC 66
VHL/E 67 TGTGTCCTCACCGACGTGCTTAATCAGTCGAAG 99
VHL/E 100 CCAGTCACGTTGTTTCTGTACGGCGTTGTCTTT 132
VHL/E 133 CTCTTCGGTTCCATCGGCAACTTCTTGGTGATC 165
VHL/E 166 TTCACCATCACCTGGCGACGTCGGATTCAATGT 198
VHL/E 199 TCCGGCGATGTTTACTTTATCAACCTCGCGGCC 231
VHL/E 232 GCCGATTTGCTTTTCGTTTGTACACTACCTCTG 264
VHL/E 265 TGGATGCAATACCTCCTAGATCACAACTCCCTA 297
VHL/E 298 GCCAGCGTGCCGTGTACGTTACTCACTGCCTGT 330
VHL/E 331 TTCTACGTGGCTATGTTTGCCAGTTTGTGTTTT 363
VHL/E 364 ATCACGGAGATTGCACTCGATCGCTACTACGCT 396
VHL/E 397 ATTGTTTACATGAGATATCGGCCTGTAAAACAG 429
VHL/E 430 GCCTGCCTTTTCAGTATTTTTTGGTGGATCTTT 462
VHL/E 463 GCCGTGATCATCGCCATTCCACACTTTATGGTG 495
VHL/E 496 GTGACCAAAAAAGACAATCAATGTATGACCGAC 528
VHL/E 529 TACGACTACTTAGAGGTCAGTTACCCGATCATC 561
VHL/E 562 CTCAACGTAGAACTCATGCTCGGTGCTTTCGTG 594
VHL/E 595 ATCCCGCTCAGTGTCATCAGCTACTGCTACTAC 627
VHL/E 628 CGCATTTCCAGAATCGTTGCGGTGTCTCAGTCG 660
VHL/E 661 CGCCACAAAGGCCGCATTGTACGGGTACTTATA 693
VHL/E 694 GCGGTCGTGCTTGTCTTTATCATCTTTTGGCTG 726
VHL/E 727 CCGTACCACCTGACGCTGTTTGTGGACACGTTG 759
VHL/E 760 AAACTGCTCAAATGGATCTCCAGCAGCTGCGAG 792
VHL/E 793 TTCGAAAAATCACTCAAGCGCGCGCTCATCTTG 825
VHL/E 826 ACCGAGTCACTCGCCTTTTGTCACTGTTGTCTC 858
VHL/E 859 AATCCGCTGCTGTACGTCTTCGTGGGCACCAAG 891
VHL/E 892 TTTCGGCAAGAACTGCACTGTCTGCTGGCCGAG 924
VHL/E 925 TTTCGCCAGCGACTGTTTTCCCGCGATGTATCC 957
VHL/E 958 TGGTACCACAGCATGAGCTTTTCGCGTCGGAGC 990
VHL/E 991 TCGCCGAGCCGAAGAGAGACGTCTTCCGACACG 1023
VHL/E 1024 CTGTCCGACGAGGCGTGTCGCGTCTCACAAATT 1056
VHL/E 1057 ATACCGTAA 1065

Fig. 1A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VHL/E 34 PVTLFLYGVVFLFGSIGNFLVIFTITWRRRIQC 66
VHL/E 67 SGDVYFINLAAADLLFVCTLPLWMQYLLDHNSL 98
VHL/E 100 ASVPCTLLTACFYVAMFASLCFITEIALDRYYA 132
VHL/E 133 IVYMRYRPVKQACLFSIFWWIFAVIIAIPHFMV 165
VHL/E 166 VTKKDNQCMTDYDYLEVSYPIILNVELMLGAFV 198
VHL/E 199 IPLSVISYCYYRISRIVAVSQSRHKGRIVRVLI 231
VHL/E 232 AVVLVFIIFWLPYHLTLFVDTLKLLKWISSSCE 264
VHL/E 265 FEKSLKRALILTESLAFCHCCLNPLLYVFVGTK 297
VHL/E 298 FRQELHCLLAEFRQRLFSRDVSWYHSMSFSRRS 330
VHL/E 331 SPSRRETSSDTLSDEACRVSQIIP 354

Fig. 1B

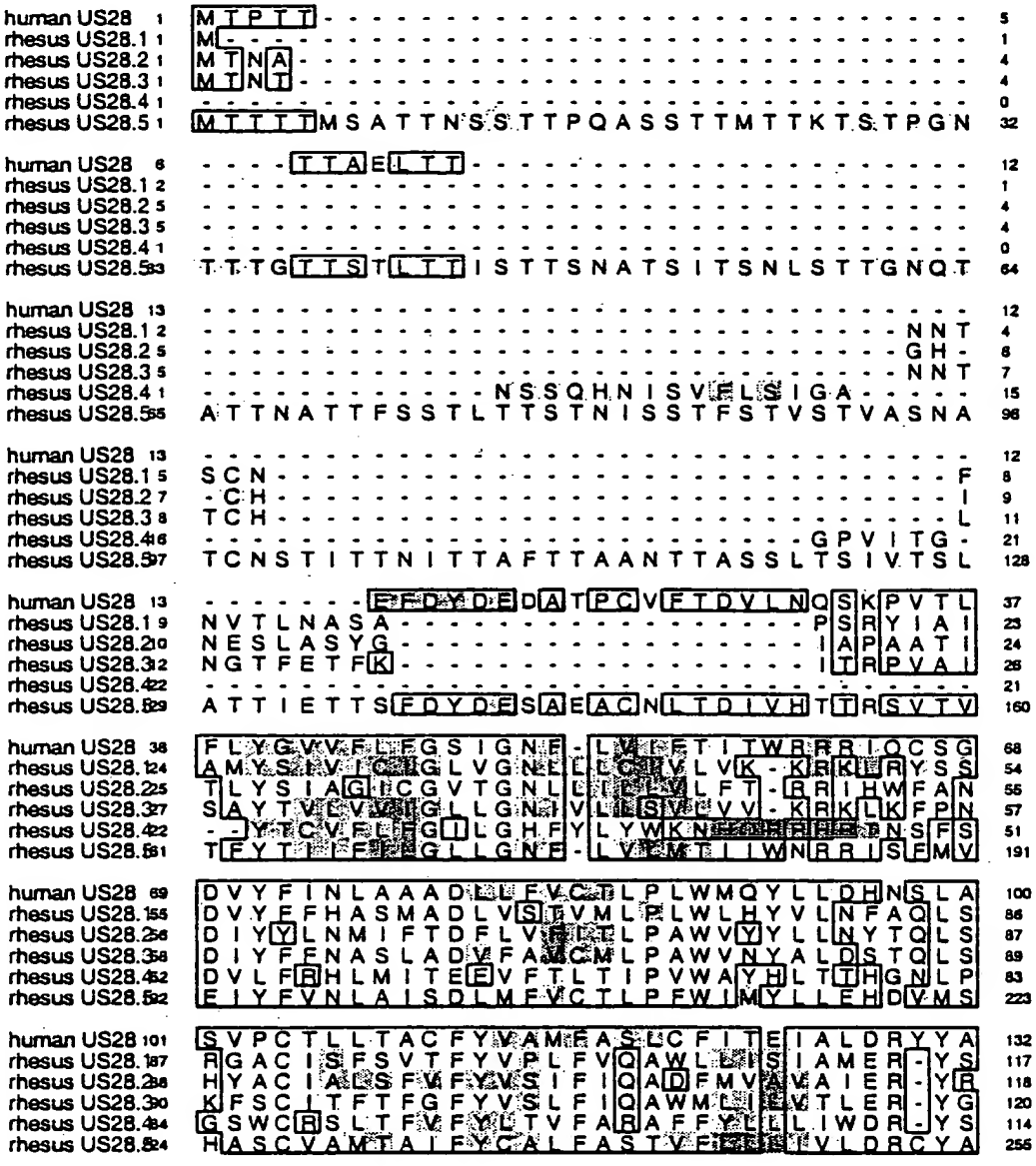

FIG. 2 (Page 1 of 2)

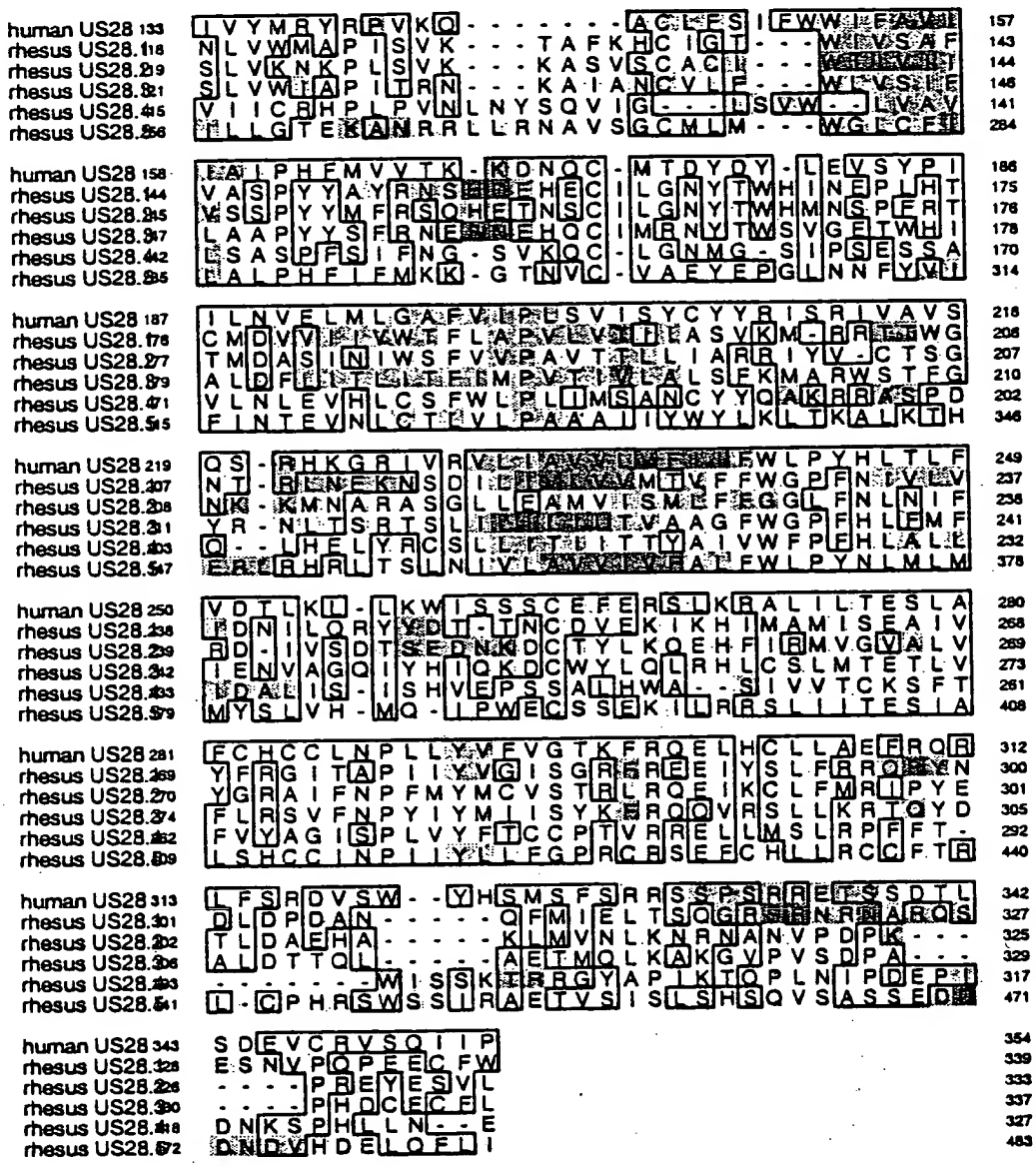

FIG. 2 (Page 2 of 2)

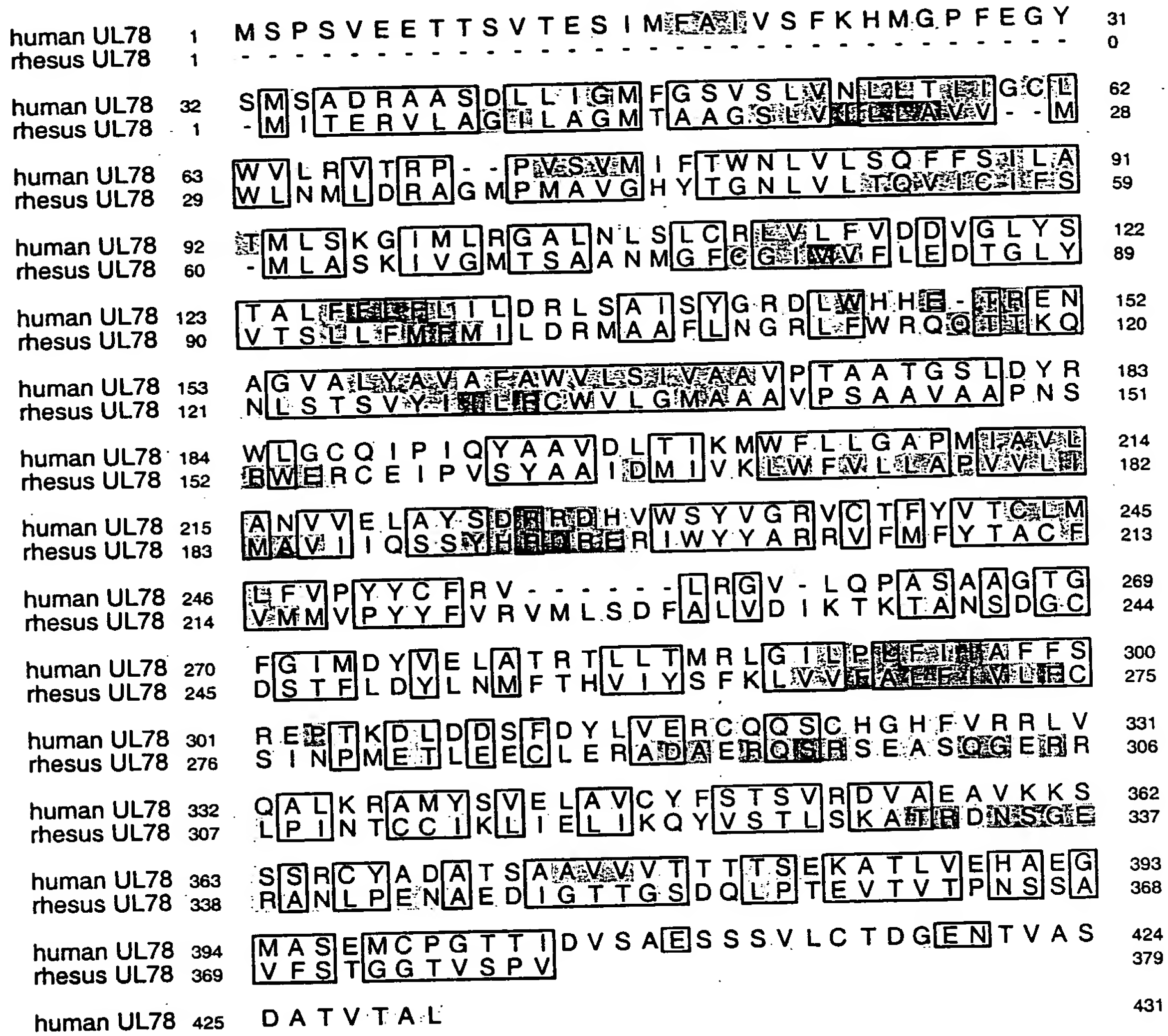
human UL78 1 M S P S V E E T T S V T E S I M E A I V S F K H M G P F E G Y 31
rhesus UL78 1 - 0
human UL78 32 S M S A D R A A S D L L I G M F G S V S L V N L E T L I G C L 62
rhesus UL78 1 - M I T E R V L A G F L A G M T A A G S L V K F L D A V V - - M 28
human UL78 63 W V L R V T R P - - P V S V M I F T W N L V L S Q F F S I L A 91
rhesus UL78 29 W L N M L D R A G M P M A V G H Y T G N L V L T Q V I C I F S 59
human UL78 92 T M L S K G I M L R G A L N L S L C R E V L F V D D V G L Y S 122
rhesus UL78 60 - M L A S K I V G M T S A A N M G F C G I W V F L E D T G L Y 89
human UL78 123 T A L F I E R F L I L D R L S A I S Y G R D L W H H E - T R E N 152
rhesus UL78 90 V T S L L F M R M I L D R M A A F L N G R L F W R Q Q T T K Q 120
human UL78 153 A G V A L Y A V A F A W V L S I V A A V P T A A T G S L D Y R 183
rhesus UL78 121 N L S T S V Y I S L L R C W V L G M A A A V P S A A V A A P N S 151
human UL78 184 W L G C Q I P I Q Y A A V D L T I K M W F L L G A P M I A V L 214
rhesus UL78 152 R W E R C E I P V S Y A A I D M I V K L W F V L L A P V V L H 182
human UL78 215 A N V V E L A Y S D R R D H V W S Y V G R V C T F Y V T C L M 245
rhesus UL78 183 M A V I I Q S S Y H R D R E R I W Y Y A R R V F M F Y T A C F 213
human UL78 246 L F V P Y Y C F R V - - - - - - L R G V - L Q P A S A A G T G 269
rhesus UL78 214 V M M V P Y Y F V R V M L S D F A L V D I K T K T A N S D G C 244
human UL78 270 F G I M D Y V E L A T R T L L T M R L G I L P L F I L A F F S 300
rhesus UL78 245 D S T F L D Y L N M F T H V I Y S F K L V V F A A F F V L F C 275
human UL78 301 R E R T K D L D D S F D Y L V E R C Q Q S C H G H F V R R L V 331
rhesus UL78 276 S I N P M E T L E E C L E R A D A E R Q S R S E A S Q G E R R 306
human UL78 332 Q A L K R A M Y S V E L A V C Y F S T S V R D V A E A V K K S 362
rhesus UL78 307 L P I N T C C I K L I E L I K Q Y V S T L S K A T R D N S G E 337
human UL78 363 S S R C Y A D A T S A A V V V T T T T S E K A T L V E H A E G 393
rhesus UL78 338 R A N L P E N A E D I G T T G S D Q L P T E V T V T P N S S A 368
human UL78 394 M A S E M C P G T T I D V S A E S S S V L C T D G E N T V A S 424
rhesus UL78 369 V F S T G G T V S P V 379
human UL78 425 D A T V T A L 431

FIG. 3

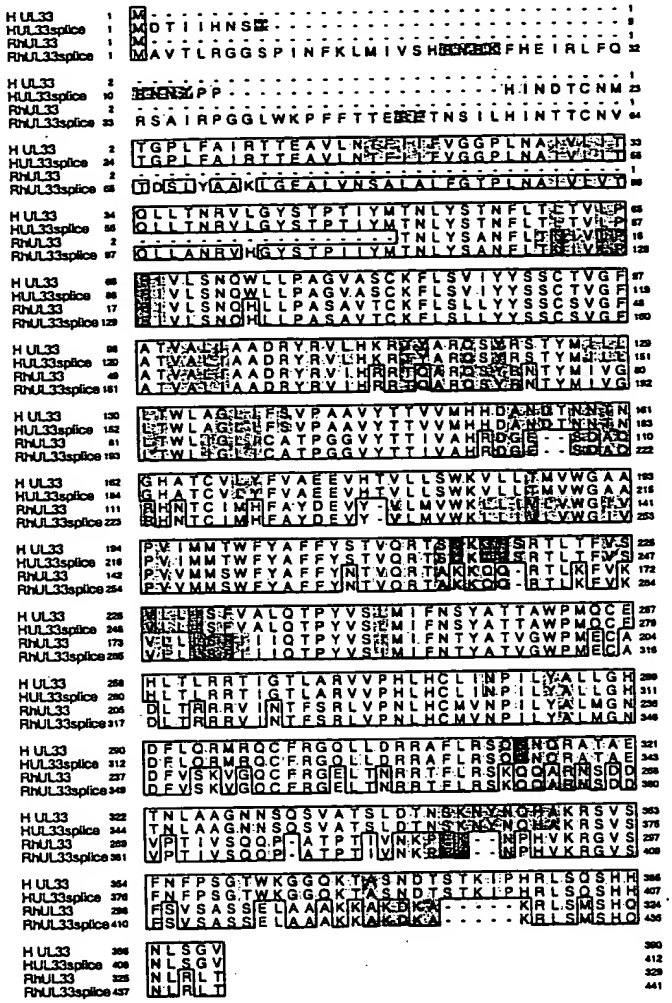

FIG. 4

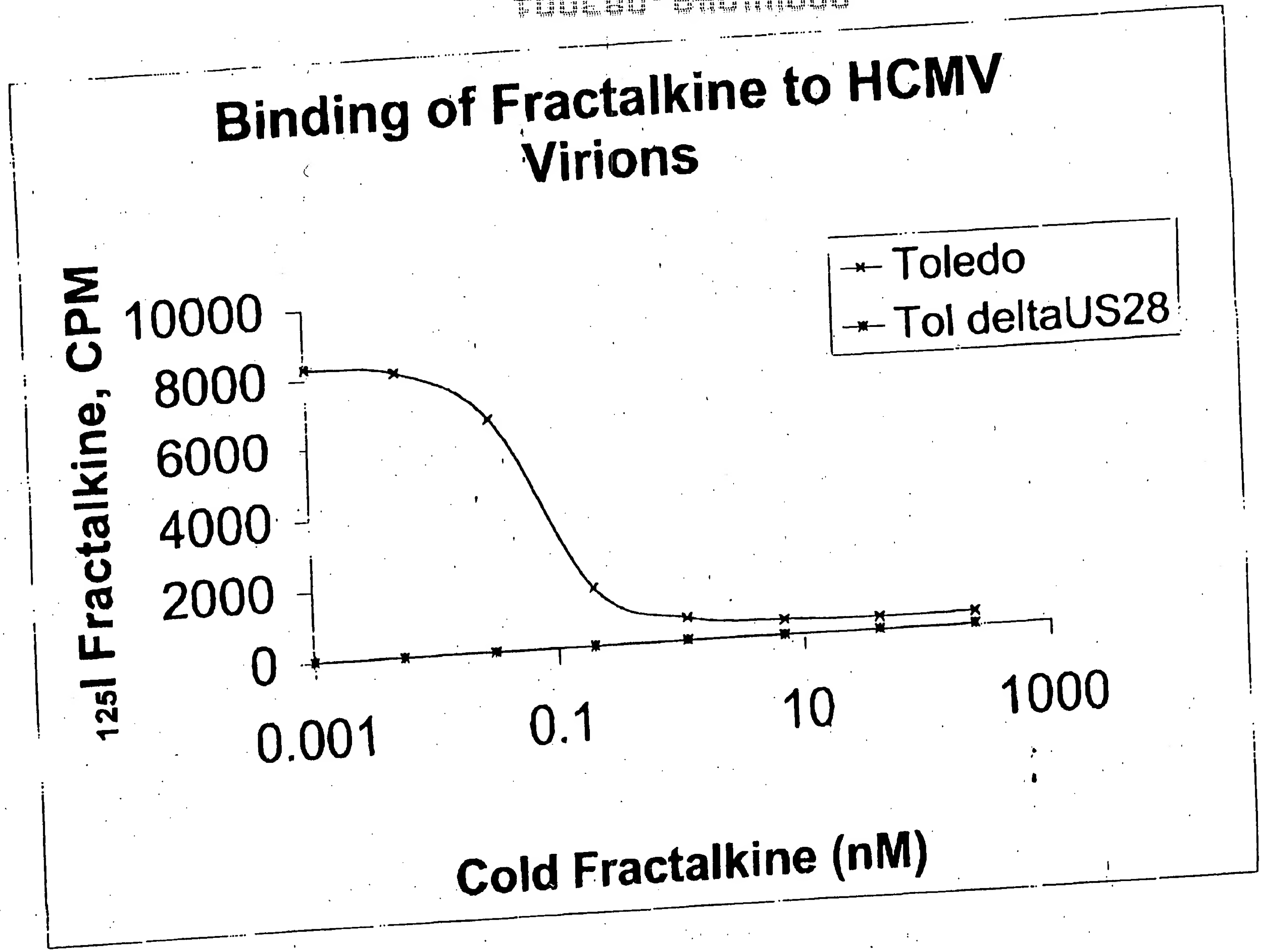
Binding of Fractalkine to HCMV Virions
Toledo
Tol deltaUS28
10000
8000
6000
4000
2000
0
125I Fractalkine, CPM
0.001
0.1
10
1000
Cold Fractalkine (nM)

FIG. 5

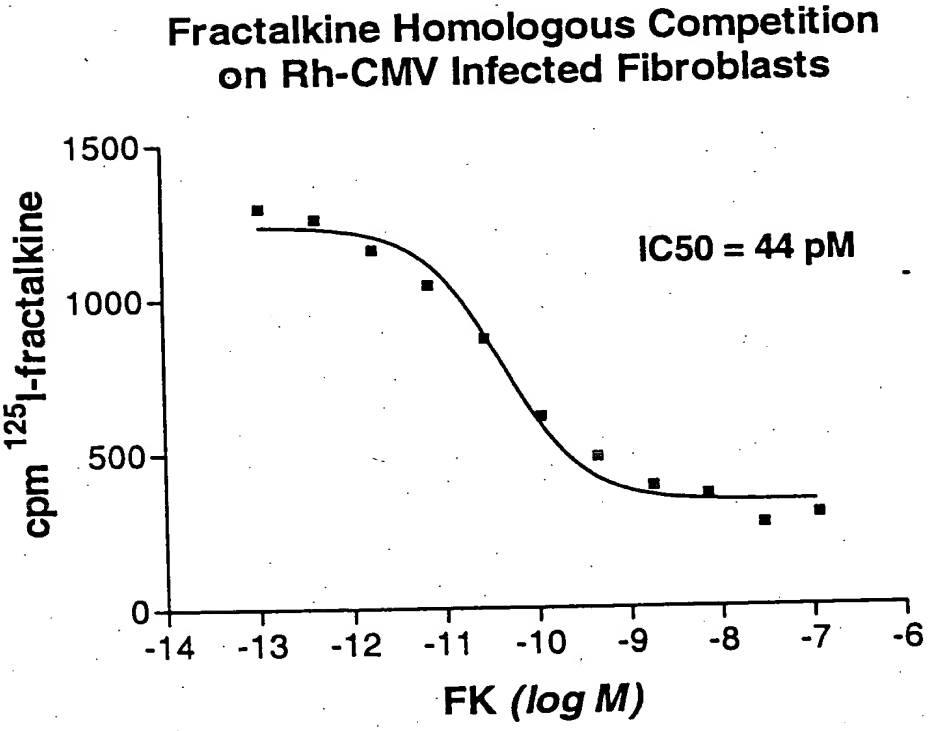
Fractalkine Homologous Competition
on Rh-CMV Infected Fibroblasts
cpm 125I-fractalkine
1500
1000
500
0
IC50 = 44 pM
-14
-13
-12
-11
-10
-9
-8
-7
-6
FK (log M)

FIG. 6

Sucrose Virions/CX3C binding

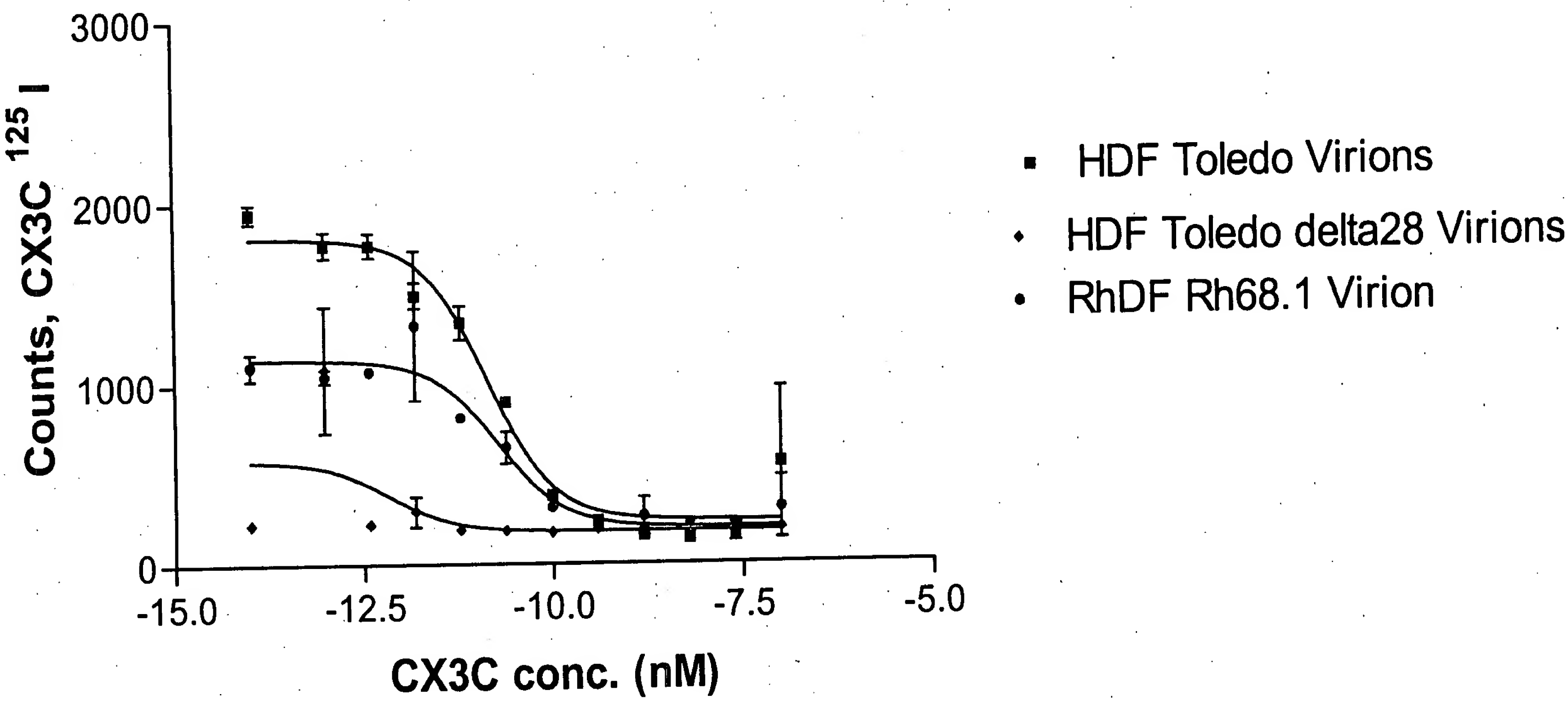

FIG. 7